

## CLAIMS

We claim:

1. An isolated nucleic acid molecule comprising a polynucleotide selected from the group consisting of:

- (a) a polynucleotide encoding amino acids from about 1 to about 273 of SEQ ID NO:2;
- (b) a polynucleotide encoding amino acids from about 2 to about 273 of SEQ ID NO:2;
- (c) a polynucleotide encoding amino acids from about 26 to about 273 of SEQ ID NO:2;
- (d) the polynucleotide complement of the polynucleotide of (a), (b), or (c); and
- (e) a polynucleotide at least 90% identical to the polynucleotide of (a), (b), (c), or (d).

2. An isolated nucleic acid molecule comprising 24-738 contiguous nucleotides from the coding region of SEQ ID NO:1.

3. The isolated nucleic acid molecule of claim 2, which comprises 50-500 contiguous nucleotides from the coding region of SEQ ID NO:1.

4. The isolated nucleic acid molecule of claim 3, which comprises 75-250 contiguous nucleotides from the coding region of SEQ ID NO:1.

5. An isolated nucleic acid molecule comprising a polynucleotide encoding a polypeptide wherein, except for at least one conservative amino acid substitution, said polypeptide has an amino acid sequence selected from the group consisting of:

- (a) amino acids about 1 to about 273 of SEQ ID NO:2;
- (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
- (c) amino acids 26 to 273 of SEQ ID NO:2.

6. The isolated nucleic acid molecule of claim 1, which is DNA.

7. A method of making a recombinant vector comprising inserting a nucleic acid molecule of claim 1 into a vector in operable linkage to a promoter.

8. A recombinant vector produced by the method of claim 7.

9. A method of making a recombinant host cell comprising introducing the recombinant vector of claim 8 into a host cell.

10. A recombinant host cell produced by the method of claim 9.

11. A recombinant method of producing a polypeptide, comprising culturing the recombinant host cell of claim 10 under conditions such that said polypeptide is expressed and recovering said polypeptide.

12. An isolated polypeptide comprising amino acids at least 95% identical to amino acids selected from the group consisting of:

- (a) amino acids about 1 to about 273 of SEQ ID NO:2;
- (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
- (c) amino acids 26 to 273 of SEQ ID NO:2.

13. An isolated polypeptide wherein, except for at least one conservative amino acid substitution, said polypeptide has an amino acid sequence selected from the group consisting of:

- (a) amino acids about 1 to about 273 of SEQ ID NO:2;
- (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
- (c) amino acids 26 to 273 of SEQ ID NO:2.

14. An isolated polypeptide comprising amino acids selected from the group consisting of:

- (a) amino acids about 1 to about 273 of SEQ ID NO:2;
- (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
- (c) amino acids 26 to 273 of SEQ ID NO:2.

15. An epitope-bearing portion of the polypeptide of SEQ ID NO:2.

16. The epitope-bearing portion of claim 15, which comprises 8-25 contiguous amino acids of SEQ ID NO:2.

17. The epitope-bearing portion of claim 15, which comprises 10 contiguous amino acids of SEQ ID NO:2.

18. An isolated antibody that binds specifically to the polypeptide of claim 12.

19. An isolated antibody that binds specifically to a polypeptide of claim 13.

20. An isolated antibody that binds specifically to the polypeptide of claim 14.

21. A method for detecting a human gene encoding SEQ ID NO:2 said method comprising obtaining in computer-readable format SEQ ID NO:1, comparing said sequence with

polynucleotide sequences of a human genome, and identifying one or more human genome sequences having at least 95% sequence identity to SEQ ID NO:1 as determined by the Smith-Waterman algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1 as parameters.

22. A non-naturally occurring fusion protein comprising a first protein segment and a second protein segment fused to each other by means of a peptide bond, wherein the first protein segment comprises at least six contiguous amino acids selected from an amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 or the complement thereof.

23. The fusion protein of claim 22 wherein said first protein segment comprises at least six contiguous amino acids of SEQ ID NO:2.

24. The fusion protein of claim 23 wherein said first protein segment comprises at least twelve contiguous amino acids of SEQ ID NO:2.

25. The fusion protein of claim 22 wherein said first protein segment comprises amino acids 20-30 of SEQ ID NO:2.

26. The fusion protein of claim 24 wherein said first protein segment comprises at least 50 contiguous amino acids of SEQ ID NO:2.

27. The fusion protein of claim 26 wherein said first protein segment comprises at least 100 contiguous amino acids of SEQ ID NO:2.

28. The fusion protein of claim 22 wherein said first protein segment comprises amino acids 26-287 of SEQ ID NO:2.

29. A method for comparing metastatic potential of tumor cells in a first and second tissue sample, comprising:

measuring in said tissue samples an expression product of a gene which comprises a polypeptide coding region of SEQ ID NO:1, wherein at least a two-fold greater expression of the product in the first tissue sample indicates a greater metastatic potential compared to the second tissue sample.

30. The method of claim 29 wherein the expression product is protein.

31. The method of claim 30 wherein the protein is measured using an antibody which specifically binds to the protein.

32. The method of claim 29 wherein the expression product is mRNA.

33. The method of claim 32 wherein said mRNA is measured using a polynucleotide probe comprising at least 20 contiguous nucleotides of nucleotides 365-1173 of SEQ ID NO:1.

34. A composition for inhibiting expression of protein by a mammary carcinoma cell, said composition comprising the polynucleotide of SEQ ID NO:4.

35. A method of inhibiting expression of a protein by a mammary carcinoma cell, said method comprising contacting said cell with a composition comprising the polynucleotide of SEQ ID NO:4.